

10/057940

(FILE 'HOME' ENTERED AT 11:06:06 ON 25 FEB 2005)

FILE 'CAPLUS, EMBASE, BIOSIS, MEDLINE, WPIDS' ENTERED AT 11:06:22 ON 25 FEB 2005

L1 158 S (PANTOLIANO, M? OR PANTOLIANO M?)/AU, IN
L2 290 S (SALEMME, F? OR SALEMME F?)/AU, IN
L3 415 S (CARVER, T? OR CARVER T?)/AU, IN
L4 470 S (3 OR THREE) (2A) (DIMENSIONAL) (2A) (PHARM?)
L5 0 S (L1 OR L2 OR L3) AND L4
L6 5 S L1 AND L2 AND L3
L7 2 DUP REM L6 (3 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 11:10:21 ON 25 FEB 2005

FILE 'CAPLUS, EMBASE, BIOSIS, MEDLINE, WPIDS' ENTERED AT 11:13:12 ON 25 FEB 2005

L8 59 S (L1 OR L2 OR L3) AND PROTEIN? AND CLASSIF?
L9 58 DUP REM L8 (1 DUPLICATE REMOVED)
L10 1017 S (LIGAND?) (3A) (CONFORMATION?) (3A) (PROTEIN?)
L11 1 S L10 AND (PROTEIN? OR KINASE) (3A) (CLASSIFY? OR CLASSIFICATION?)
L12 1593 S (CLASSIFY OR CLASSIFICATION?)/TI
L13 104579 S (CLASSIFY OR CLASSIFICATION?)/TI
L14 1828 S L13 AND (PROTEIN?)/TI
L15 0 S L10 AND L14
L16 1 S L14 AND (THERMAL OR HEAT) (3A) (DENATURAT? OR SHIFT? OR CONFORM
L17 1063 S L13 AND ASSAY?
L18 0 S L17 AND (DENATURATION OR DENATURE)
L19 46 S L17 AND LIGAND?
L20 23 DUP REM L19 (23 DUPLICATES REMOVED)

=>

L7 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
AN 2002:74444 CAPLUS
DN 137:163756
TI High-density miniaturized thermal shift assays as a general strategy for
drug discovery
AU Pantoliano, Michael W.; Petrella, Eugene C.; Kwasnoski, Joseph
D.; Lobanov, Victor S.; Myslik, James; Graf, Edward; Carver, Ted
; Asel, Eric; Springer, Barry A.; Lane, Pamela; Salemme, F. R.
CS 3-Dimensional Pharmaceuticals, Inc., Exton, PA, USA
SO Journal of Biomolecular Screening (2001), 6(6), 429-440
CODEN: JBISF3; ISSN: 1087-0571
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB More general and universally applicable drug discovery assay technologies
are needed in order to keep pace with the recent advances in combinatorial
chemical and genomics-based target generation. Ligand-induced conformational
stabilization of proteins is a well-understood phenomenon in which
substrates, inhibitors, cofactors, and even other proteins provide
enhanced stability to proteins on binding. This phenomenon is based on
the energetic coupling of the ligand-binding and protein-melting
reactions. In an attempt to harness these biophys. properties for drug
discovery, fully automated instrumentation was designed and implemented to
perform miniaturized fluorescence-based thermal shift assays in a
microplate format for the high throughput screening of compound libraries.
Validation of this process and instrumentation was achieved by
investigating ligand binding to more than 100 protein targets. The
general applicability of the thermal shift screening strategy was found to
be an important advantage because it circumvents the need to design and
retool new assays with each new therapeutic target. Moreover, the
miniaturized thermal shift assay methodol. does not require any prior
knowledge of a therapeutic target's function, making it ideally suited for
the quant. high throughput drug screening and evaluation of targets
derived from genomics.
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

WEST Search History

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DATE: Friday, February 25, 2005

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,DWPI; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L3	L2 same (panel or panels)	44
<input type="checkbox"/>	L2	L1 same protein	2712
<input type="checkbox"/>	L1	fingerprint\$	30804

END OF SEARCH HISTORY

10/057,940

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Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
	<i>DB=USPT,DWPI; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L11	L10 and (classify or classification or class)near4(protein\$ or kinase\$)	15
<input type="checkbox"/>	L10	(thermal)near2(shift)	922
<input type="checkbox"/>	L9	(classify or classification or kinase\$)near2(protein)near5(stability or denaturation or folding)	18
<input type="checkbox"/>	L8	L7 and (classify or classification)	43
<input type="checkbox"/>	L7	(modify or modification or change or changing)near2(protein)near5(stability or denaturation or folding)	598
<input type="checkbox"/>	L6	(denatur\$).clm. and (classif\$).clm.	12
<input type="checkbox"/>	L5	L4 and (classif\$).clm.	5
<input type="checkbox"/>	L4	(protein\$)near3(classify or classification)	139
<input type="checkbox"/>	L3	(protein\$)near3(classify or classification)near10(aggreat\$)	0
<input type="checkbox"/>	L2	(protein\$)near3(classify or classification)near5(aggreat\$)	0
<input type="checkbox"/>	L1	(protein\$)near3(classify or classification)near5(thermal or denatur\$)	5

END OF SEARCH HISTORY